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1  CGAGGCCACGGCTTATGCAAGCAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
-----+-----+-----+-----+-----+-----+-----+
61  AGATGAACTCATGACTGTACTCTACCCAGAAATATTGGAATGTACAAGTGTCAAGCTAAG
-----+-----+-----+-----+-----+-----+-----+
      M T V L Y P E Y W K M Y K C Q L R
-----+-----+-----+-----+-----+-----+-----+
121 GAAAGGAGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
-----+-----+-----+-----+-----+-----+-----+
      K G G W Q H N R E Q A N L N S R T E E T
-----+-----+-----+-----+-----+-----+-----+
181 TATAAAATTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
-----+-----+-----+-----+-----+-----+-----+
      I K F A A A H Y N T E I L K S I D N E W
-----+-----+-----+-----+-----+-----+-----+
241 GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGAGGAGTTTGGAGT
-----+-----+-----+-----+-----+-----+-----+
      R K T Q C M P R E V C I D V G K E F G V
-----+-----+-----+-----+-----+-----+-----+
301 CGGACAAACACCTTCTTTAAACCTCCATGTGTGTCCTACAGATGTGGGGTTCCTG
-----+-----+-----+-----+-----+-----+-----+
      A T N T F F K P P C V S V Y R C G C C C
-----+-----+-----+-----+-----+-----+-----+
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FIG. 2A

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1081 TCGTGTGTCCCTTCATATTGGCAAGACCACAAATGAGCTAAGATTGTACTGTTTCCCA
      R C V P S Y W Q R P Q M S
1141 GTTCATCGATTTTCTATTATGGAAACTGTGTGGCCACAGTAGAACTGTCTGTGAACAGA
1201 GAGACCCCTTGTGGTCCATGCTAACAAAGACAAAGTCTGTCTTTCCTGAACCATGTGGA
1261 TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCCTCTTGTAAGACTGGTTT
1321 CTGCCAATGACCAACAGCCCAAGATTTTCCCTCTGTGATTTCTTTAAAGAATGACTATA
1381 TAATTTATTTCCACTAAAATAATTGTTTCTGCAATTCATTTTATAGCAACAACAATTGGT
1441 AAACTCACTGTGATCAATAATTTTATATCATGCAAAATATGTTTAAATAAATGAAAAA
1501 TTGTATTTATAAAAAAATAAAAAA
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FIG. 2D